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1278—A60

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Commercial Relationships: B. Dugas, Jr., None; **C. Fourgeux, Jr.**, None; **B. Buteau, Jr.**, None; **L. Martine, Jr.**, None; **I. Björkhem, Sr.**, None; **N. Acar, Sr.**, None; **A. Bron, Sr.**, None; **F. Nicot, Jr.**, None; **C. Creuzot-Garcher, Sr.**, None; **L. Bretillon, Sr.**, None.

Support: None.

Clinical Trial: www.clinicaltrials.gov NCT00629044

Abstract

Purpose: To estimate the association and interaction of single nucleotide polymorphism (SNP) in cholesterol-24S-hydroxylase (CYP46A1) gene with HTRA1, LOC387715, CFH SNPs with age-related macular degeneration (AMD) in a North-East French population.

Methods: Cross-sectional study involving 142 AMD patients with exudative AMD or geographic atrophy and 70 unrelated control subjects. SNPs were genotyped in CYP46A1, HTRA1, LOC387715, and CFH genes. Plasma 24S-hydroxycholesterol, the metabolic product of CYP46A1, was quantified. Sex, age, alleles, and genotype frequencies between AMD patients and controls were compared using the χ^2 and Student t-tests. Odd-ratios (OR) and 95% confidence intervals (CI) were calculated by logistic regression to assess the relative association between disease and age, sex, and genotypes.

Results: The SNP rs754203 in CYP46A1 was not associated with AMD (OR=1.1, 95% CI=0.78-1.43, p=0.76). The OR for risk of AMD was 2.1 (95% CI=1.1-4.4, p=0.03) for the A-allele of rs11200638 in HTRA1, 2.8 (95% CI=1.4-5.5, p=0.002) for the T-allele of rs10490924 in LOC387715, and 1.5 (95% CI=1.1-2.0, p=0.004) for the C-allele for rs1061170 in CFH. These associations were found only in patients with exudative AMD but not with geographic atrophy. An OR of 11.3 (95% CI=0.7-170, p=0.003) was obtained for carriers with both CC-genotype in CFH and TT in CYP46A1.

Conclusions: The TT-genotype of rs754203 in CYP46A1 conferred a higher risk for exudative AMD in patients who carry the CC-genotype of rs1061170 in CFH.

Keywords: age-related macular degeneration • choroid: neovascularization • genetics